LLSSYO

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ALTMNI

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320 LLMHLG

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ALTERNATE_NAMES

TITLE

ENTRY

RESULT

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                                                                                                                                                                                                                                                                             196
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              *binding_site carbohydrate (Asn) (covalent) *status
#domain transmembrane #status predicted #label TM7\
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     WTPYNIVILLNTEQEF-FGLSNCESTSQLDQAFQVTETLGMTHCCINPIIYAFVGEKFRR
                                                                                                                                                                                                                                                                                                                           -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF
                                                                                                                                                                                                                                                                                                                                                                      YSWRHFHTLRMTIFCLVLPLLVMAICYTGI1KTLLRCPS-KKKYKAIRLIFVIMAVFFIF
                                                                                                                                                                                                                                                                                                           VTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV
                                                                                                                                                                                                                                                                            VTFGVVTSVÍTÝLVA/FASVPGIIFTKCOKEDSVYVCGPYFP--R-
                                                                                                                                                                                                                                              LLNLAISDLLFLVTLPFWIHKVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLT PDRY
                                                                                                                                       TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINGKKLKCLTDIY
                                                                                                                                                                                   TSYYD-DVGLLCEKADTRALMAOFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIY\mathcal{T}\mathcal{M}3 ' \mathcal{T}\mathcal{M}3 ' '
                                                             #checksum 1732
                                                                                                                                                                                                     LENDAISDLEFLITEPEWAHFA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTH
                                                                                                                                                                                                                                 Length 360;
                                                                                                                           Indels
                                                                                                                                                                        311 YLRHFFHRHLLMHLGRYIPFLPSEKLE-RTSSVSPSTAEPELS 352
                                                 #disulfide_bonds #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLSVFFRKHITKRFCKOCPVFYRETVDGVTSTNTPSTGEQEVS
                                                             #length 360 #molecular-weight 41063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 5.17e-187;
                                                                                             Score 1438; DB 2;
                                                                                                                                                                                                                                                                                               87; Mismatches
                                                                                                                                                                                                                                  predicted
                                                                                                 52.0%;
                                                                                                            53.4%;
                                                                                                                             Conservative ECI
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                                                                                                                                                                                                                                                                                                                 LAIVHAVFALRART
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                                                                      SUMMARY
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##residue ##cross-r ##CIOSS-I #map_positic KEYWORDS #cross-refer ##molecul ##status #accession #authors #journal ACCESSIONS REFERENCE #title GENETICS #dene ORGANISM DATE

> 10 ORGANISM RESULT TITLE ENTRY DATE

02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change #formal_name Mus musculus #common_name house mouse - monse MIP-1 alpha receptor like-1 #type complete I49340